

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Ullrich, Axel
Risau, Werner
Millauer, Birgit
Gazit, Aviv
Levitzki, Alex
- (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular Endothelial Growth Factor
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pennie & Edmonds
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/193,829
 - (B) FILING DATE: 09-FEB-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-060
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 286..4386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT	60
CGAATTGGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCGGCG	120
ACACCGCTGA CAGCCGCAGC TGGAGCCAGG GCGCCGGTGC CCCCGCCTCT CCCCGGTCTT	180
GCGCTGCCGG GGCCATACCG CCTCTGTGAC TTCTTGCGG GCCAGGGACG GAGAAGGAGT	240
CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GGCGCGAGGT GCAGG ATG GAG AGC Met Glu Ser	294
1	
AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC	342
Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala	
5 10 15	
GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC	390
Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser	
20 25 30 35	
ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT	438
Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile	
40 45 50	
ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG	486
Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln	
55 60 65	
CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC	534
Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp	
70 75 80	
AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT	582
Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp	
85 90 95	
ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT	630
Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr	
100 105 110 115	
GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC	678
Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val	
120 125 130	
AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT	726
Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr	
135 140 145	
GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT	774
Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu	
150 155 160	
TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT	822
Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile	
165 170 175	
TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC	870
Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser	
180 185 190 195	

TAT	GCC	GGC	ATG	GTC	TTC	TGT	GAG	GCA	AAG	ATC	AAT	GAT	GAA	ACC	TAT	918
Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Thr	Tyr	
				200				205							210	
CAG	TCT	ATC	ATG	TAC	ATA	GTT	GTG	GTT	GTA	GGA	TAT	AGG	ATT	TAT	GAT	966
Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	
				215				220							225	
GTG	ATT	CTG	AGC	CCC	CCG	CAT	GAA	ATT	GAG	CTA	TCT	GCC	GGA	GAA	AAA	1014
Val	Ile	Leu	Ser	Pro	Pro	His	Glu	Ile	Glu	Leu	Ser	Ala	Gly	Glu	Lys	
				230				235							240	
CTT	GTC	TTA	AAT	TGT	ACA	GCG	AGA	ACA	GAG	CTC	AAT	GTG	GGG	CTT	GAT	1062
Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Leu	Asp	
				245				250							255	
TTC	ACC	TGG	CAC	TCT	CCA	CCT	TCA	AAG	TCT	CAT	CAT	AAG	AAG	ATT	GTA	1110
Phe	Thr	Trp	His	Ser	Pro	Pro	Ser	Lys	Ser	His	His	Lys	Lys	Ile	Val	
				260				265							275	
AAC	CGG	GAT	GTG	AAA	CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	1158
Asn	Arg	Asp	Val	Lys	Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	
				280				285							290	
AGC	ACC	TTG	ACA	ATA	GAA	AGT	GTG	ACC	AAG	AGT	GAC	CAA	GGG	GAA	TAC	1206
Ser	Thr	Leu	Thr	Ile	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln	Gly	Glu	Tyr	
				295				300							305	
ACC	TGT	GTA	GCG	TCC	AGT	GGA	CGG	ATG	ATC	AAG	AGA	AAT	AGA	ACA	TTT	1254
Thr	Cys	Val	Ala	Ser	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn	Arg	Thr	Phe	
				310				315							320	
GTC	CGA	GTT	CAC	ACA	AAG	CCT	TTT	ATT	GCT	TTC	GGT	AGT	GGG	ATG	AAA	1302
Val	Arg	Val	His	Thr	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser	Gly	Met	Lys	
				325				330							335	
TCT	TTG	GTG	GAA	GCC	ACA	GTG	GGC	AGT	CAA	GTC	CGA	ATC	CCT	GTG	AAG	1350
Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile	Pro	Val	Lys	
				340				345							355	
TAT	CTC	AGT	TAC	CCA	GCT	CCT	GAT	ATC	AAA	TGG	TAC	AGA	AAT	GGA	AGG	1398
Tyr	Leu	Ser	Tyr	Pro	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg	Asn	Gly	Arg	
				360				365							370	
CCC	ATT	GAG	TCC	AAC	TAC	ACA	ATG	ATT	GTT	GGC	GAT	GAA	CTC	ACC	ATC	1446
Pro	Ile	Glu	Ser	Asn	Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu	Leu	Thr	Ile	
				375				380							385	
ATG	GAA	GTG	ACT	GAA	AGA	GAT	GCA	GGA	AAC	TAC	ACG	GTC	ATC	CTC	ACC	1494
Met	Glu	Val	Thr	Glu	Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val	Ile	Leu	Thr	
				390				395							400	
AAC	CCC	ATT	TCA	ATG	GAG	AAA	CAG	AGC	CAC	ATG	GTC	TCT	CTG	GTT	GTG	1542
Asn	Pro	Ile	Ser	Met	Glu	Lys	Gln	Ser	His	Met	Val	Ser	Leu	Val	Val	
				405				410							415	
AAT	GTC	CCA	CCC	CAG	ATC	GGT	GAG	AAA	GCC	TTG	ATC	TCG	CCT	ATG	GAT	1590
Asn	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser	Pro	Met	Asp	
				420				425							435	
TCC	TAC	CAG	TAT	GGG	ACC	ATG	CAG	ACA	TTG	ACA	TGC	ACA	GTC	TAC	GCC	1638

Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala 440 445 450	
AAC CCT CCC CTG CAC CAC ATC CAG TGG TAC TGG CAG CTA GAA GAA GCC Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu Glu Glu Ala 455 460 465	1686
TGC TCC TAC AGA CCC GGC CAA ACA AGC CCG TAT GCT TGT AAA GAA TGG Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp 470 475 480	1734
AGA CAC GTG GAG GAT TTC CAG GGG GGA AAC AAG ATC GAA GTC ACC AAA Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys 485 490 495	1782
AAC CAA TAT GCC CTG ATT GAA GGA AAA AAC AAA ACT GTA AGT ACG CTG Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu 500 505 510 515	1830
GTC ATC CAA GCT GCC AAC GTG TCA GCG TTG TAC AAA TGT GAA GCC ATC Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile 520 525 530	1878
AAC AAA GCG GGA CGA GGA GAG AGG GTC ATC TCC TTC CAT GTG ATC AGG Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg 535 540 545	1926
GGT CCT GAA ATT ACT GTG CAA CCT GCT GCC CAG CCA ACT GAG CAG GAG Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu 550 555 560	1974
AGT GTG TCC CTG TTG TGC ACT GCA GAC AGA AAT ACG TTT GAG AAC CTC Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu 565 570 575	2022
ACG TGG TAC AAG CTT GGC TCA CAG GCA ACA TCG GTC CAC ATG GGC GAA Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His Met Gly Glu 580 585 590 595	2070
TCA CTC ACA CCA GTT TGC AAG AAC TTG GAT GCT CTT TGG AAA CTG AAT Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn 600 605 610	2118
GGC ACC ATG TTT TCT AAC AGC ACA AAT GAC ATC TTG ATT GTG GCA TTT Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe 615 620 625	2166
CAG AAT GCC TCT CTG CAG GAC CAA GGC GAC TAT GTT TGC TCT GCT CAA Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln 630 635 640	2214
GAT AAG AAG ACC AAG AAA AGA CAT TGC CTG GTC AAA CAG CTC ATC ATC Asp Lys Lys Thr Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile 645 650 655	2262
CTA GAG CGC ATG GCA CCC ATG ATC ACC GGA AAT CTG GAG AAT CAG ACA Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu Asn Gln Thr 660 665 670 675	2310
ACA ACC ATT GGC GAG ACC ATT GAA GTG ACT TGC CCA GCA TCT GGA AAT Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn	2358

680	685	690	
CCT ACC CCA CAC ATT ACA TGG TTC AAA GAC AAC GAG ACC CTG GTA GAA Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu 695 700 705			2406
GAT TCA GGC ATT GTA CTG AGA GAT GGG AAC CGG AAC CTG ACT ATC CGC Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu Thr Ile Arg 710 715 720			2454
AGG GTG AGG AAG GAG GAT GGA GGC CTC TAC ACC TGC CAG GCC TGC AAT Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln Ala Cys Asn 725 730 735			2502
GTC CTT GGC TGT GCA AGA GCG GAG ACG CTC TTC ATA ATA GAA GGT GCC Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile Glu Gly Ala 740 745 750 755			2550
CAG GAA AAG ACC AAC TTG GAA GTC ATT ATC CTC GTC GGC ACT GCA GTG Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly Thr Ala Val 760 765 770			2598
ATT GCC ATG TTC TTC TGG CTC CTT CTT GTC ATT GTC CTA CGG ACC GTT Ile Ala Met Phe Phe Trp Leu Leu Val Ile Val Leu Arg Thr Val 775 780 785			2646
AAG CGG GCC AAT GAA GGG GAA CTG AAG ACA GGC TAC TTG TCT ATT GTC Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val 790 795 800			2694
ATG GAT CCA GAT GAA TTG CCC TTG GAT GAG CGC TGT GAA CGC TTG CCT Met Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro 805 810 815			2742
TAT GAT GCC AGC AAG TGG GAA TTC CCC AGG GAC CGG CTG AAA CTA GGA Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly 820 825 830 835			2790
AAA CCT CTT GGC CGC GGT GCC TTC GGC CAA GTG ATT GAG GCA GAC GCT Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala 840 845 850			2838
TTT GGA ATT GAC AAG ACA GCG ACT TGC AAA ACA GTA GCC GTC AAG ATG Phe Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met 855 860 865			2886
TTG AAA GAA GGA GCA ACA CAC AGC GAG CAT CGA GCC CTC ATG TCT GAA Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu 870 875 880			2934
CTC AAG ATC CTC ATC CAC ATT GGT CAC CAT CTC AAT GTG GTG AAC CTC Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu 885 890 895			2982
CTA GGC GCC TGC ACC AAG CCG GGA GGG CCT CTC ATG GTG ATT GTG GAA Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu 900 905 910 915			3030
TTC TGC AAG TTT GGA AAC CTA TCA ACT TAC TTA CGG GGC AAG AGA AAT Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn 920 925 930			3078

GAA TTT GTT CCC TAT AAG AGC AAA GGG GCA CGC TTC CGC CAG GGC AAG Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys 935 940 945	3126
GAC TAC GTT GGG GAG CTC TCC GTG GAT CTG AAA AGA CGC TTG GAC AGC Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser 950 955 960	3174
ATC ACC AGC AGC CAG AGC TCT GCC AGC TCA GGC TTT GTT GAG GAG AAA Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys 965 970 975	3222
TCG CTC AGT GAT GTA GAG GAA GAA GAA GCT TCT GAA GAA CTG TAC AAG Ser Leu Ser Asp Val Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys 980 985 990 995	3270
GAC TTC CTG ACC TTG GAG CAT CTC ATC TGT TAC AGC TTC CAA GTG GCT Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala 1000 1005 1010	3318
AAG GGC ATG GAG TTC TTG GCA TCA AGG AAG TGT ATC CAC AGG GAC CTG Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu 1015 1020 1025	3366
GCA GCA CGA AAC ATT CTC CTA TCG GAG AAG AAT GTG GTT AAG ATC TGT Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys 1030 1035 1040	3414
GAC TTC GGC TTG GCC CGG GAC ATT TAT AAA GAC CCG GAT TAT GTC AGA Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg 1045 1050 1055	3462
AAA GGA GAT GCC CGA CTC CCT TTG AAG TGG ATG GCC CCG GAA ACC ATT Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile 1060 1065 1070 1075	3510
TTT GAC AGA GTA TAC ACA ATT CAG AGC GAT GTG TGG TCT TTC GGT GTG Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val 1080 1085 1090	3558
TTG CTC TGG GAA ATA TTT TCC TTA GGT GCC TCC CCA TAC CCT GGG GTC Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val 1095 1100 1105	3606
AAG ATT GAT GAA GAA TTT TGT AGG AGA TTG AAA GAA GGA ACT AGA ATG Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met 1110 1115 1120	3654
CGG GCT CCT GAC TAC ACT ACC CCA GAA ATG TAC CAG ACC ATG CTG GAC Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp 1125 1130 1135	3702
TGC TGG CAT GAG GAC CCC AAC CAG AGA CCC TCG TTT TCA GAG TTG GTG Cys Trp His Glu Asp Pro Asn Gln Arg Pro Ser Phe Ser Glu Leu Val 1140 1145 1150 1155	3750
GAG CAT TTG GGA AAC CTC CTG CAA GCA AAT GCG CAG CAG GAT GGC AAA Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys 1160 1165 1170	3798
GAC TAT ATT GTT CTT CCA ATG TCA GAG ACA CTG AGC ATG GAA GAG GAT	3846

Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met Glu Glu Asp	1175	1180	1185	
TCT GGA CTC TCC CTG CCT ACC TCA CCT GTT TCC TGT ATG GAG GAA GAG	1190	1195	1200	3894
Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu				
GAA GTG TGC GAC CCC AAA TTC CAT TAT GAC AAC ACA GCA GGA ATC AGT	1205	1210	1215	3942
Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser				
CAT TAT CTC CAG AAC AGT AAG CGA AAG AGC CGG CCA GTG AGT GTA AAA	1220	1225	1230	3990
His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys				
1235				
ACA TTT GAA GAT ATC CCA TTG GAG GAA CCA GAA GTA AAA GTG ATC CCA	1240	1245	1250	4038
Thr Phe Glu Asp Ile Pro Leu Glu Pro Glu Val Lys Val Ile Pro				
GAT GAC AGC CAG ACA GAC AGT GGG ATG GTC CTT GCA TCA GAA GAG CTG	1255	1260	1265	4086
Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu				
1270	1275	1280		
AAA ACT CTG GAA GAC AGG AAC AAA TTA TCT CCA TCT TTT GGT GGA ATG				4134
Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe Gly Gly Met				
1285	1290	1295		
ATG CCC AGT AAA AGC AGG GAG TCT GTG GCC TCG GAA GGC TCC AAC CAG				4182
Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln				
1300	1305	1310	1315	
ACC AGT GGC TAC CAG TCT GGG TAT CAC TCA GAT GAC ACA GAC ACC ACC				4230
Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr				
1320	1325	1330		
GTG TAC TCC AGC GAC GAG GCA GGA CTT TTA AAG ATG GTG GAT GCT GCA				4278
Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val Asp Ala Ala				
1335	1340	1345		
GTT CAC GCT GAC TCA GGG ACC ACA CTG CAG CTC ACC TCC TGT TTA AAT				4326
Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser Cys Leu Asn				
1350	1355	1360		
GGA AGT GGT CCT GTC CCG GCT CCG CCC CCA ACT CCT GGA AAT CAC GAG				4374
Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly Asn His Glu				
1365				
AGA GGT GCT GCT TAGATTTCAG AGTGTGTTTC TTTCCACCAAC CCGGAAGTAG				4426
Arg Gly Ala Ala				
CCACATTTGA TTTTCATTT TGGAGGAGGG ACCTCAGACT GCAAGGAGCT TGTCTCAGG				4486
GCATTTCCAG AGAAGATGCC CATGACCAA GAATGTGTTG ACTCTACTCT CTTTCCATT				4546
CATTTAAAG TCCTATATAA TGTGCCCTGC TGTGGTCTCA CTACCAGTTA AAGCAAAAGA				4606
CTTTCAAACA CGTGGACTCT GTCCTCCAAG AAGTGGCAAC GGCACCTCTG TGAAACTGGA				4666
TCGAATGGGC AATGCTTGT GTGTTGAGGA TGGGTGAGAT GTCCCAGGGC CGAGTCTGTC				4726

TACCTTGGAG GCTTTGTGGA GGATGCAGGC TATGAGCCAA GTGTTAAGTG TGGGATGTGG	4786
ACTGGGAGGA AGGAAGGCGC AAGTCGCTCG GAGAGCGGTT GGAGCCTGCA GATGCATTGT	4846
GCTGGCTCTG GTGGAGGTGG GCTTGTGGCC TGTCAAGGAAA CGCAAAGGCG GCCGGCAGGG	4906
TTTGGTTTG GAAGGTTTGC GTGCTCTTCA CAGTCGGGTT ACAGGCGAGT TCCCTGTGGC	4966
TTTCCTACT CCTAATGAGA GTTCCTTCCG GACTCTTACG TGTCTCCTGG CCTGGCCCCA	5026
GGAAGGAAAT GATGCAGCTT GTCCTTCCT CATCTCTCAG GCTGTGCCTT AATTCAAGAAC	5086
ACCAAAAGAG AGGAACGTCG GCAGAGGCTC CTGACGGGGC CGAAGAATTG TGAGAACAGA	5146
ACAGAAACTC AGGGTTTCTG CTGGGTGGAG ACCCACGTGG CGCCCTGGTG GCAGGTCTGA	5206
GGGTTCTCTG TCAAGTGGCG GTAAAGGCTC AGGCTGGTGT TCTTCCTCTA TCTCCACTCC	5266
TGTCAGGCC CCAAGTCCTC AGTATTTAG CTTTGTGGCT TCCTGATGGC AGAAAAATCT	5326
TAATTGGTTG GTTGCTCTC CAGATAATCA CTAGCCAGAT TTGAAATTAA CTTTTTAGCC	5386
GAGGTTATGA TAACATCTAC TGTATCCTT AGAATTTAA CCTATAAAAC TATGTCTACT	5446
GGTTTCTGCC TGTGTGCTTA TGTT	5470

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1367 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu			
1	5	10	15
Thr Arg Ala Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro			
20	25	30	
Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr			
35	40	45	
Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro			
50	55	60	
Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly			
65	70	75	80
Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val			
85	90	95	
Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile			
100	105	110	
Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile			
115	120	125	

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
210 215 220

Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225 230 235 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
245 250 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
260 265 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
275 280 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
290 295 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305 310 315 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
325 330 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
340 345 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
355 360 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
370 375 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385 390 395 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
405 410 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
420 425 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450	455	460
Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys		
465	470	475
Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu		
485	490	495
Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val		
500	505	510
Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys		
515	520	525
Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His		
530	535	540
Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr		
545	550	555
560		
Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe		
565	570	575
Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His		
580	585	590
Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp		
595	600	605
Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile		
610	615	620
Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys		
625	630	635
640		
Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln		
645	650	655
Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu		
660	665	670
Asn Gln Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala		
675	680	685
Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr		
690	695	700
Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu		
705	710	715
720		
Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln		
725	730	735
Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile		
740	745	750
Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly		
755	760	765
Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu		
770	775	780

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785 790 795 800

Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu
805 810 815

Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu
820 825 830

Lys Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu
835 840 845

Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala
850 855 860

Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu
865 870 875 880

Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val
885 890 895

Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val
900 905 910

Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly
915 920 925

Lys Arg Asn Glu Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg
930 935 940

Gln Gly Lys Asp Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg
945 950 955 960

Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val
965 970 975

Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Ala Ser Glu Glu
980 985 990

Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe
995 1000 1005

Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His
1010 1015 1020

Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val
1025 1030 1035 1040

Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp
1045 1050 1055

Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met Ala Pro
1060 1065 1070

Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val Trp Ser
1075 1080 1085

Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr
1090 1095 1100

Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly

1105 1110 1115 1120
Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr
1125 1130 1135
Met Leu Asp Cys Trp His Glu Asp Pro Asn Gln Arg Pro Ser Phe Ser
1140 1145 1150
Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln
1155 1160 1165
Asp Gly Lys Asp Tyr Ile Val Leu Pro Met Ser Glu Thr Leu Ser Met
1170 1175 1180
Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser Cys Met
1185 1190 1195 1200
Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn Thr Ala
1205 1210 1215
Gly Ile Ser His Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg Pro Val
1220 1225 1230
Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu Val Lys
1235 1240 1245
Val Ile Pro Asp Asp Ser Gln Thr Asp Ser Gly Met Val Leu Ala Ser
1250 1255 1260
Glu Glu Leu Lys Thr Leu Glu Asp Arg Asn Lys Leu Ser Pro Ser Phe
1265 1270 1275 1280
Gly Gly Met Met Pro Ser Lys Ser Arg Glu Ser Val Ala Ser Glu Gly
1285 1290 1295
Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp Asp Thr
1300 1305 1310
Asp Thr Thr Val Tyr Ser Ser Asp Glu Ala Gly Leu Leu Lys Met Val
1315 1320 1325
Asp Ala Ala Val His Ala Asp Ser Gly Thr Thr Leu Gln Leu Thr Ser
1330 1335 1340
Cys Leu Asn Gly Ser Gly Pro Val Pro Ala Pro Pro Pro Thr Pro Gly
1345 1350 1355 1360
Asn His Glu Arg Gly Ala Ala
1365

(3) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCATGGATC TTCTGTTAA

18

(4) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGTACAAGT ATAAGTAGTA GCCCAGGTAC CAG

33

(5) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Ser Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro
20 25 30

Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly
65 70 75 80

Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val
85 90 95

Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile
100 105 110

Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile
115 120 125

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp
195 200 205

Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg
210 215 220

Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225 230 235 240

Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
245 250 255

Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
260 265 270

Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
275 280 285

Met Phe Leu Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
290 295 300

Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305 310 315 320

Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
325 330 335

Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
340 345 350

Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
355 360 365

Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
370 375 380

Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385 390 395 400

Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
405 410 415

Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
420 425 430

Pro Met Asp Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu

450 455 460

Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys
465 470 475 480

Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu
485 490 495

Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val
500 505 510

Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys
515 520 525

Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His
530 535 540

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr
545 550 555 560

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe
565 570 575

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His
580 585 590

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp
595 600 605

Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile
610 615 620

Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys
625 630 635 640

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln
645 650 655

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu
660 665 670

Asn Gln Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala
675 680 685

Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr
690 695 700

Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu
705 710 715 720

Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln
725 730 735

Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile
740 745 750

Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly
755 760 765

Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu
770 775 780

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785 790 795 800

Ser Ile Val Met Asp Pro

(6) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly
1 5 10 15

Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys
20 25 30

Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu Phe
35 40 45

Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr
50 55 60

Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr
65 70 75 80

Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu
85 90 95

Ser Asp Val Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp Phe
100 105 110

Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly
115 120 125

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
130 135 140

Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe
145 150 155 160

Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
165 170 175

Asp Ala Arg Leu
180